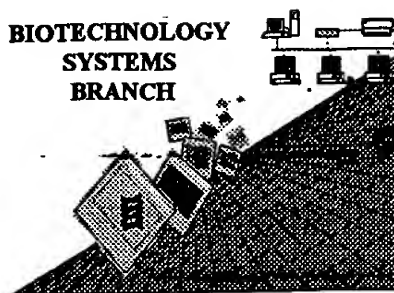


Raw

RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/262,126

Source: 1682

Date Processed by STIC: 9/14/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

1652

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/262,126

DATE: 09/14/2000
TIME: 10:27:41

Input Set : A:\GC396-2 seq.txt
Output Set: N:\CRF3\09142000\I262126.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Miller, Brian S.
4 Shetty, Jayarama K.
6 <120> TITLE OF INVENTION: Modified Forms of Pullulanase
9 <130> FILE REFERENCE: GC396-2
11 <140> CURRENT APPLICATION NUMBER: 09/262,126
12 <141> CURRENT FILING DATE: 1999-03-03
14 <160> NUMBER OF SEQ ID NOS: 9
16 <170> SOFTWARE: FastSEQ for Windows Version 3.0

ERRORED SEQUENCES

306 <210> SEQ ID NO: 4
307 <211> LENGTH: 1091
308 <212> TYPE: PRT
309 <213> ORGANISM: K. pneumonia
311 <400> SEQUENCE: 4
312 Met Leu Arg Tyr Thr Arg Asn Ala Leu Val Leu Gly Ser Leu Val Leu
313 1 5 10 15
314 Leu Ser Gly Cys Asp Asn Gly Ser Ser Ser Ser Ser Ser Gly Asn
315 20 25 30
316 Pro Asp Thr Pro Asp Asn Gln Asp Val Val Val Arg Leu Pro Asp Val
317 35 40 45
318 Ala Val Pro Gly Glu Ala Val Thr Ala Val Glu Asn Gln Ala Val Ile
319 50 55 60
320 His Leu Val Asp Ile Ala Gly Ile Thr Ser Ser Ser Ala Ala Asp Tyr
321 65 70 75 80
322 Ser Ser Lys Asn Leu Tyr Leu Trp Asn Asn Glu Thr Cys Asp Ala Leu
323 85 90 95
324 Ser Ala Pro Val Ala Asp Trp Asn Asp Val Ser Thr Thr Pro Ser Gly
325 100 105 110
326 Ser Asp Lys Tyr Gly Pro Tyr Trp Val Ile Pro Leu Asn Lys Glu Ser
327 115 120 125
328 Gly Cys Ile Asn Val Ile Val Arg Asp Gly Thr Asp Lys Leu Ile Asp
329 130 135 140
330 Ser Asp Leu Arg Val Ala Phe Gly Asp Phe Thr Asp Arg Thr Val Ser
331 145 150 155 160
332 Val Ile Ala Gly Asn Ser Ala Val Tyr Asp Ser Arg Ala Asp Ala Phe
333 165 170 175
334 Arg Ala Ala Phe Gly Val Ala Leu Ala Glu Ala His Trp Val Asp Lys
335 180 185 190
336 Asn Thr Leu Leu Trp Pro Gly Gly Gln Asp Lys Pro Ile Val Arg Leu
337 195 200 205
338 Tyr Tyr Ser His Ser Ser Lys Val Ala Ala Asp Gly Glu Gly Lys Phe
339 210 215 220
340 Thr Asp Arg Tyr Leu Lys Leu Thr Pro Thr Thr Val Ser Gln Gln Val
341 225 230 235 240

seq. 4

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/262,126

DATE: 09/14/2000
 TIME: 10:27:41

Input Set : A:\GC396-2 seq.txt
 Output Set: N:\CRF3\09142000\I262126.raw

```

342 Ser Met Arg Phe Pro His Leu Ser Ser Tyr Ala Ala Phe Lys Leu Pro
343           245           250           255
344 Asp Asn Ala Asn Val Asp Glu Leu Leu Gln Gly Glu Thr Val Ala Ile
345           260           265           270
346 Ala Ala Ala Glu Asp Gly Ile Leu Ile Ser Ala Thr Gln Val Gln Thr
347           275           280           285
348 Ala Gly Val Leu Asp Asp Ala Tyr Ala Glu Ala Ala Glu Ala Leu Ser
349           290           295           300
350 Tyr Gly Ala Gln Leu Ala Asp Gly Gly Val Thr Phe Arg Val Trp Ala
351           305           310           315           320
352 Pro Thr Ala Gln Gln Val Asp Val Val Val Tyr Ser Ala Asp Lys Lys
353           325           330           335
354 Val Ile Gly Ser His Pro Met Thr Arg Asp Ser Ala Ser Gly Ala Trp
355           340           345           350
356 Ser Trp Gln Gly Gly Ser Asp Leu Lys Gly Ala Phe Tyr Arg Tyr Ala
357           355           360           365
358 Met Thr Val Tyr His Pro Gln Ser Arg Lys Val Glu Gln Tyr Glu Val
359           370           375           380
360 Thr Asp Pro Tyr Ala His Ser Leu Ser Thr Asn Ser Glu Tyr Ser Gln
361           385           390           395           400
362 Val Val Asp Leu Asn Asp Ser Ala Leu Lys Pro Asp Gly Trp Asp Asn
363           405           410           415
364 Leu Thr Met Pro His Ala Gln Lys Thr Lys Ala Asp Leu Ala Lys Met
365           420           425           430
366 Thr Ile His Glu Ser His Ile Arg Asp Leu Ser Ala Trp Asp Gln Thr
367           435           440           445
368 Val Pro Ala Glu Leu Arg Gly Lys Tyr Leu Ala Leu Thr Ala Gly Asp
369           450           455           460
370 Ser Asn Met Val Gln His Leu Lys Thr Leu Ser Ala Ser Gly Val Thr
371           465           470           475           480
372 His Val Glu Leu Leu Pro Val Phe Asp Leu Ala Thr Val Asn Glu Phe
373           485           490           495
374 Ser Asp Lys Val Ala Asp Ile Gln Gln Pro Phe Ser Arg Leu Cys Glu
375           500           505           510
376 Val Asn Ser Ala Val Lys Ser Ser Glu Phe Ala Gly Tyr Cys Asp Ser
377           515           520           525
378 Gly Ser Thr Val Glu Glu Val Leu Asn Gln Leu Lys Gln Ser Asp Ser
379           530           535           540
380 Gln Asp Asn Pro Gln Val Gln Ala Leu Asn Thr Leu Val Ala Gln Thr
381           545           550           555           560
382 Asp Ser Tyr Asn Trp Gly Tyr Asp Pro Phe His Tyr Thr Val Pro Glu
383           565           570           575
384 Gly Ser Tyr Ala Thr Asp Pro Glu Gly Thr Thr Arg Ile Lys Glu Phe
385           580           585           590
386 Arg Thr Met Ile Gln Ala Ile Lys Gln Asp Leu Gly Met Asn Val Ile
387           595           600           605
388 Met Asp Val Val Tyr Asn His Thr Asn Ala Ala Gly Pro Thr Asp Arg
389           610           615           620
390 Thr Ser Val Leu Asp Lys Ile Val Pro Trp Tyr Tyr Gln Arg Leu Asn

```

RAW SEQUENCE LISTING

DATE: 09/14/2000

PATENT APPLICATION: US/09/262,126

TIME: 10:27:41

Input Set : A:\GC396-2 seq.txt

Output Set: N:\CRF3\09142000\I262126.raw

```

391 625 630 635 640
392 Glu Thr Thr Gly Ser Val Glu Ser Ala Thr Cys Cys Ser Asp Ser Ala
393 645 650 655
394 Pro Glu His Arg Met Phe Ala Lys Leu Ile Ala Asp Ser Leu Ala Val
395 660 665 670
396 Trp Thr Thr Asp Tyr Lys Ile Asp Gly Phe Arg Phe Asp Leu Met Gly
397 675 680 685
398 Tyr His Pro Lys Ala Gln Ile Leu Ser Ala Trp Glu Arg Ile Lys Ala
399 690 695 700
400 Leu Asn Pro Asp Ile Tyr Phe Phe Gly Glu Gly Trp Asp Ser Asn Gln
401 705 710 715 720
402 Ser Asp Arg Phe Glu Ile Ala Ser Gln Ile Asn Leu Lys Gly Thr Gly
403 725 730 735
404 Ile Gly Thr Phe Ser Asp Arg Leu Arg Asp Ser Val Arg Gly Gly Gly
405 740 745 750
406 Pro Phe Asp Ser Gly Asp Ala Leu Arg Gln Asn Gln Gly Ile Gly Ser
407 755 760 765
408 Gly Ala Gly Val Leu Pro Asn Glu Leu Ala Ser Leu Ser Asp Asp Gln
409 770 775 780
410 Val Arg His Leu Ala Asp Leu Thr Arg Leu Gly Met Ala Gly Asn Leu
411 785 790 795 800
412 Ala Asp Phe Val Met Ile Asp Lys Asp Gly Ala Ala Lys Lys Gly Ser
413 805 810 815
414 Glu Ile Asp Tyr Asn Gly Ala Pro Gly Gly Tyr Ala Ala Asp Pro Thr
415 820 825 830
416 Glu Val Val Asn Tyr Val Ser Lys His Asp Asn Gln Thr Leu Trp Asp
417 835 840 845
418 Met Ile Ser Tyr Lys Ala Ser Gln Glu Ala Asp Leu Ala Thr Arg Val
419 850 855 860
420 Arg Met Gln Ala Val Ser Leu Ala Thr Val Met Leu Gly Gln Gly Ile
421 865 870 875 880
422 Ala Phe Asp Gln Gln Gly Ser Glu Leu Leu Arg Ser Lys Ser Phe Thr
423 885 890 895
424 Arg Asp Ser Tyr Asp Ser Gly Asp Trp Phe Asn Arg Val Asp Tyr Ser
425 900 905 910
426 Leu Gln Asp Asn Asn Tyr Asn Val Gly Met Pro Arg Ile Ser Asp Asp
427 915 920 925
428 Gly Ser Asn Tyr Glu Val Ile Thr Arg Val Lys Glu Met Val Ala Thr
429 930 935 940
430 Pro Gly Glu Ala Glu Leu Lys Gln Met Thr Ala Phe Tyr Gln Glu Leu
431 945 950 955 960
432 Thr Glu Leu Arg Lys Ser Ser Pro Leu Phe Thr Leu Gly Asp Gly Ser
433 965 970 975
434 Ala Val Met Lys Arg Val Asp Phe Arg Asn Thr Gly Ser Asp Gln Gln
435 980 985 990
436 Ala Gly Leu Leu Val Met Thr Val Asp Asp Gly Met Lys Ala Gly Ala
437 995 1000 1005
438 Ser Leu Asp Ser Arg Leu Asp Gly Leu Val Val Ala Ile Asn Ala Ala
439 1010 1015 1020

```

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/262,126

DATE: 09/14/2000
 TIME: 10:27:41

Input Set : A:\GC396-2 seq.txt
 Output Set: N:\CRF3\09142000\I262126.raw

```

440 Pro Glu Ser Arg Thr Leu Asn Glu Phe Ala Gly Glu Thr Leu Gln Leu
E--> 441 1025          1030          1035          ← 1040
442 Ser Ala Ile Gln Gln Thr Ala Gly Glu Asn Ser Leu Ala Asn Gly Val
443          1045          1050          1055
444 Gln Ile Ala Ala Asp Gly Thr Val Thr Leu Pro Ala Trp Ser Val Ala
445          1060          1065          1070
446 Val Leu Glu Leu Pro Gln Gly Glu Ala Gln Gly Ala Gly Leu Pro Val
447          1075          1080          1085
448 Ser Ser Lys
449          1090

```

when numbering the
 last amino acid on
 a line, end the
 number under the
last letter of
 the amino acid.
 (e.g. ^{Leu} 1040)

Otherwise, the last
 number will be
 cut off in the
 processed sequence
 listing.

See next page for more errors

09/262,126

5

<210> 1
 <211> 2794
 <212> DNA
 <213> B. deramificans

<400> 1

gatgggaaca	cgacaacgat	cattgtccac	tatttttggc	ctgctgggtga	ttatcaacct	60
tggagtctat	ggatgtggcc	aaaagacgga	ggtggggctg	aatacgattt	caatcaaccg	120
gctgactctt	ttggagctgt	tgcaagtgt	gatattccag	gaaacccaag	tcaggtagga	180
attatcgttc	gcactcaaga	ttggaccaaa	gatgtgagcg	ctgaccgcta	catagattta	240
agcaaaggaa	atgaggtgtg	gcttgtagaa	ggaaacagcc	aaatTTTTTT	taatgaaaaa	300
gatgctgagg	atgcagctaa	acccgctgta	agcaacgctt	atttagatgc	ttcaaaccag	360
gtgctggtta	aacttagcca	gccgttaact	cttgggggaag	gnnnAagcgg	ctttacgggt	420
catgacgaca	cagcaaataa	ggatattcca	gtgacatctg	tgaaggatgc	aagtcttggt	480
caagatgtaa	ccgctgtttt	ggcagggtacc	ttccaacata	TTTTTggagg	ttccgattgg	540
gcacctgata	atcacagtac	tttattaaaa	aaggtgacta	acaatctcta	tcaattctca	600
ggagatcttc	ctgaaggaaa	ctaccaatat	aaagtggctt	taaattgatag	ctggaataat	660
ccgagttacc	catctgacaa	cattaattta	acagtccttg	ccggcgggtg	acacgtcact	720
ttttcgtata	ttccgtccac	tcatgcagtc	tatgacacaa	ttataaatcc	taatgcggat	780
ttacaagtag	aaagcggggg	taaaacggat	ctcgtgacgg	ttactctagg	ggaagatcca	840
gatgtgagcc	atactctgtc	cattcaaaca	gatggctatc	aggcaaagca	ggtgatacct	900
cgtaatgtgc	ttaattcatt	acagtactac	tattcaggag	atgatcttgg	gaatacctat	960
acacagaaag	caacaacctt	taaagtctgg	gcaccaactt	ctactcaagt	aaatgttctt	1020
ctttatgaca	gtgcaacggg	ttctgttaaca	aaaatcgtac	ctatgacggc	atcggggccat	1080
ggtgtgtggg	aagcaacggg	taatcaaaac	cttgaaaatt	ggtattacat	gtatgaggta	1140
acaggccaag	gctctaccgg	aacggctggt	gaccccttat	caactgcat	tgcaccaa	1200
ggaacgagag	gcatgattgt	ggacctggct	aaaacagatc	ctgctggctg	gaacagtgat	1260
aaacatatta	cgccaaagaa	tatagaagat	gaggtcatct	atgaaatgga	tgtccgtgac	1320
ttttccattg	accctaattc	gggtatgaaa	aataaaggga	agtatttggc	tcttacagaa	1380
aaaggaacaa	agggccctga	caacgtaaag	acgggggatag	attccttaaa	acaacttggg	1440
attactcatg	ttcagcttat	gcctgttttc	gcatctaaca	gtgtcgatga	aactgatcca	1500
accaagata	attgggggta	tgaccctcgc	aactatgatg	ttcctgaagg	gcagtatgct	1560
acaaatgcga	atggtaatgc	tcgtataaaa	gagtttaagg	aaatggttct	ttcaactccat	1620
cgtgaacaca	ttgggggttaa	catggatggt	gtctataatc	atacctttgc	cacgcaaate	1680
tctgacttcg	ataaaattgt	accagaatat	tattaccgta	cgatgatcca	ggtaattata	1740
ccaacggatc	aggtactgga	aatgaaattg	caagcggaaa	ggccaatggg	tcaaaaattt	1800
attattgatt	cccttaagta	ttgggtcaat	gagtatcata	ttgacggcct	ccgttttgac	1860
ttaatggcgc	tgcttggaag	agacacgatg	tccaaagctg	cctcggagct	tcatgctatt	1920
aatccaggaa	ttgcacttta	cgggtagcca	tggacgggtg	gaacctctgc	actgccagat	1980
gatcagcttc	tgacaaaagg	agctcaaaaa	ggcatgggag	tagcgggtgt	taatgacaat	2040
ttacgaaacg	cgttgagcgg	caatgtcttt	gattcttccg	ctcaaggttt	tgcgacaggt	2100
gcaacaggct	taactgatgc	aattaagaat	ggcgttgagg	ggagtattaa	tgactttacc	2160
tcttcaccag	gtgagacaat	taactatgtc	acaagtcatt	ataactacac	cctttgggac	2220
aaaatagccc	taagcaatcc	taatgattcc	gaagcggatc	ggattaaaat	ggatgaaact	2280
gcacaagcag	ttgttatgac	ctcacaaggc	gttccattca	tgcaaggcgg	ggaagaaatg	2340
cttcgtatga	aaggcggcaa	cgacaatagt	tataatgcag	gcgatgcggg	caatgagttt	2400
gattggagca	ggaaagctca	atatccagat	gttttcaact	attatagcgg	gctaatccac	2460
cttcgtcttg	atcaccacgc	cttcgcgatg	acgacagcta	atgaaatcaa	tagccacctc	2520
caattcctaa	atagtccaga	gaacacagtg	gcctatgaat	taactgatca	tgttaataaaa	2580
gacaaatggg	gaaatatcat	tgttgtttat	aacccaaata	aaactgtagc	aacctcaat	2640
ttgccgagcg	ggaaatgggc	aatcaatgct	acgagcggta	aggtaggaga	atccacctt	2700
ggtcaagcag	agggaagtgt	ccaagtacca	ggtatatcta	tgatgatcct	tcatcaagag	2760
gtaagccag	accacggtaa	aaagtaatat	aaaa			2794

See
 Jan
 10
 oh
 Enn
 Summary
 sheet

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/262,126

DATE: 09/14/2000
TIME: 10:27:42

Input Set : A:\GC396-2 seq.txt
Output Set: N:\CRF3\09142000\I262126.raw

L:30 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:30 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:30 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:30 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:30 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
L:53 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:53 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:53 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:53 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
M:340 Repeated in SeqNo=1
L:63 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:63 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:63 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:63 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:108 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:164 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:188 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:206 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:441 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/262126

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

RECEIVED
SEP 22 2000
TECH CENTER 1600/2900

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.